

SEQUENCE LISTING

O I P E
JUL 22 2002
TRADEMARK OFFICE 998
<110> REPKE, HEINRICH
BUDDE, ECKHARD
NICOLAUS, STEFAN

<120> PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
BEING IMMOBILIZED

<130> ALBRE-22

<140> 10/059,271
<141> 2002-01-31

<150> DE 101 06 295
<151> 2001-02-02

<160> 97

<170> PatentIn Ver. 2.1

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Gly

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1 5 10 15

Lys Xaa Gly

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Lys Xaa Xaa Cys Xaa Gly
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1 5 10 15

Arg Ala Val Gly
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<400> 5
Trp Ile Gln Leu Gln Gln Arg Leu Asn Leu Trp Gly Cys Arg Gly Lys
1 5 10 15

Leu Ile Cys Tyr Thr Asn
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<210> 6
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1 5 10 15

Leu Val Cys Tyr Thr Asn
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Leu Ile Cys Tyr Thr Asn

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Cys Ala Phe Arg Gln Val Cys Tyr
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Cys Ala Phe Arg Gln Val Cys His
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<400> 13
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<210> 14

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Thr Thr

<210> 15

<211> 19

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<400> 15

Thr Arg Gln Arg Thr Pro Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr
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Gly Gln Phe

<210> 16

<211> 18

<212> PRT

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<400> 16

Arg Thr Val Gln Glu Ile Arg Ile Gly Pro Met Ala Trp Tyr Ser Met
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Gly Ala

<210> 17

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<400> 17
Thr Met Lys Arg Thr Ser Ile His Ile Gly Pro Gly Gln Thr Phe Tyr
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Ala Thr

<210> 18
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<400> 18
Thr Arg Arg Gly Ile Pro Leu Gly Pro Gly Arg Ala Trp Tyr Ala Thr
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Leu

<210> 19
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<400> 19
Asp Ser Thr Arg Glu Ser Met Arg Ile Gly Pro Gly Gln Ala Phe Tyr
1 5 10 15

Ala Thr Gly

<210> 20
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<400> 20
Ile Arg Gln Gly Ile His Ile Gly Pro Gly Arg Ala Phe Phe Ala Ala
1 5 10 15

Trp

<210> 21
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<400> 21
Asp Val Gln Glu Met Arg Ile Gly Pro Met Ala Trp Tyr Ser Met Gly
1 5 10 15

<210> 22
<211> 20
<212> PRT
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peptide

<400> 22
Ile Cys Thr Arg Arg Gly Ile Arg Met Gly Pro Gly Gln Val Val Tyr
1 5 10 15

Ala Thr Cys Thr
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<210> 23
<211> 18
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<400> 23
Thr Ile Val Gln Ile Lys Ile Ile Gly Pro Leu Ala Val Tyr Ser Met
1 5 10 15

Tyr Gly

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<400> 24
Thr Arg Lys Ser Val Arg Ile Gly Pro Gly Gln Ala Phe Tyr Ala Thr
1 5 10 15

<210> 25

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<400> 25

Gly His Thr Arg Lys Ser Ile Arg Ile Gly Pro Gly Gln Thr Phe Tyr
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Ala Thr

<210> 26

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<400> 26

Asn Thr Arg Gln Ser Thr His Ile Gly Pro Gly Ala Leu Tyr Thr Thr
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Lys Ile Glu

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Thr Arg Lys Ser Ile His Leu Gly Pro Gly Gln Ala Phe Tyr Ala Thr
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Gly Asp

<210> 28

<211> 20

<212> PRT

<213> Artificial Sequence

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<400> 28
Tyr Gln Thr Arg Lys Ser Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr
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Ala Thr Gly Asp
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<210> 29
<211> 18
<212> PRT
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<400> 29
Thr Val Gln Glu Ile Arg Ile Gly Pro Met Ala Trp Tyr Ser Met Gly
1 5 10 15

Asn Val

<210> 30
<211> 16
<212> PRT
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<400> 30
Thr Arg Ile Ser His Thr Ile Gly Pro Gly Arg Val Phe Tyr Arg Thr
1 5 10 15

<210> 31
<211> 18
<212> PRT
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Thr Arg Lys Gly Ile His Met Gly Pro Gly Gln Val Leu Tyr Ala Thr
1 5 10 15

Lys Pro

<210> 32
<211> 18
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His Thr Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Ala
1 5 10 15

Thr Ser

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1 5 10 15

Ser Met Gln

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Gln Thr Arg Thr Ser Ile Thr Ile Gly Pro Gly Gln Val Phe Tyr Arg
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Thr Glu

<210> 35
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<400> 35
Gly Thr Arg Lys Ser Val Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala
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Thr Gly

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<400> 36
Thr Arg Lys Gly Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Thr
1 5 10 15

Gly

<210> 37
<211> 14
<212> PRT
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<400> 37
Ala Val Gly Ile Gly Ile Asn Cys Thr Arg Pro Asn Asn Asn
1 5 10

<210> 38
<211> 19
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<220>
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Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Gly Pro
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Thr Pro Thr

<210> 39
<211> 19
<212> PRT
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<220>
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<400> 39
Gly Lys Arg Ala His Lys Ser Arg Lys His Asn Tyr Lys Arg His Ile
1 5 10 15

Arg Arg Gly

<210> 40
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<212> PRT
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<220>
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<400> 40
Gly Ser Lys Lys Ala Arg Arg Ile Lys Gly Lys Met Arg Arg Leu Lys
1 5 10 15

Lys Val Gly

<210> 41
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 41
Gly Val Cys Ile Lys His Arg Tyr Lys Arg Lys Asp Lys Arg Lys His
1 5 10 15

Lys Val Ala Cys Ile Gly
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<210> 42
<211> 37
<212> DNA
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<220>
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<400> 42
atatggcata tgtttttaga tggaatagat aaggcccc

37

<210> 43
<211> 26
<212> DNA
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<400> 43
tatagggccc aggtggcagg ttaaaaa

<210> 44
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
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<400> 44
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<210> 45
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<400> 45
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<210> 46
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

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Met Phe Leu Asp Gly Ile Asp Lys Ala Gln Asp Glu His Glu Lys Tyr
1 5 10 15

His Ser Asn Trp Arg
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<210> 47
<211> 30
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Ala Met Ala Ser Asp Phe Asn Leu Pro Pro
    1           5           10

<210> 48
<211> 10
<212> PRT
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<220>
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<400> 48
Ala Met Ala Ser Asp Phe Asn Leu Pro Pro
    1           5           10

<210> 49
<211> 26
<212> DNA
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<400> 49
tatagggccc aggtggcagg ttaaaaa          26

<210> 50
<211> 47
<212> DNA
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<400> 50
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<210> 51
<211> 55
<212> DNA
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<210> 52
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<212> DNA
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<400> 52
caaaaaggcc cgtcgcata agggcaaaat gcgacgggtg aagaaag 47

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Gly Pro Lys Lys Ala Arg Arg Ile Lys Gly Lys Met Arg Arg Val Lys
1 5 10 15

Lys Ala Gly

<210> 54
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
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<400> 54
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<210> 55
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<220>
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<400> 55
taatttgcgg gcgttagtagc aaaagaaata gtag

34

<210> 56
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<212> DNA
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<400> 56
tatagcatgc tccatatgct gtttcctgcc ctgt

34

<210> 57
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
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<400> 57
taatttgcgg gcgttagtagc aaaagaaata gtag

34

<210> 58
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
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<400> 58
gtatgtacaa aagaaatagt agccagctgt gataaatgtc agctaaaagg agaagccatg 60

<210> 59
<211> 22
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<220>
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<400> 59
 Ala Gly Val Val Ala Lys Glu Ile Val Ala Ser Cys Asp Lys Cys Gln
 1 5 10 15

Leu Lys Gly Glu Ala Met
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<210> 60
 <211> 60
 <212> DNA
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<220>
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<220>
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 <222> (1)..(60)

<400> 60 48
 cat gga caa gta gac tgt agt cca gga ata tgg caa cta gat tgt aca
 His Gly Gln Val Asp Cys Ser Pro Gly Ile Trp Gln Leu Asp Cys Thr
 1 5 10 15

cat tta gaa gga 60
 His Leu Glu Gly
 20

<210> 61
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 <212> PRT
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<220>
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<400> 61 48
 His Gly Gln Val Asp Cys Ser Pro Gly Ile Trp Gln Leu Asp Cys Thr
 1 5 10 15

His Leu Glu Gly
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<210> 62
 <211> 60
 <212> DNA
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Lys Val Ile Leu Val Ala Val His Val Ala Ser Gly Tyr Ile Glu Ala
    1           5           10          15

gaa gtt att cca                                         60
Glu Val Ile Pro
    20

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<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
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<400> 63
Lys Val Ile Leu Val Ala Val His Val Ala Ser Gly Tyr Ile Glu Ala
    1           5           10          15

Glu Val Ile Pro
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<210> 64
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<400> 64
gcagaaacag ggcaggaaac agcatat                                         27

<210> 65
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<400> 65
Ala Glu Thr Gly Gln Glu Thr Ala Tyr Gly Ala Cys
    1           5           10

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<400> 66
tatagcatgc tccatatgct gtttcctgcc ctgt          34

<210> 67
<211> 56
<212> DNA
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<220>
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<400> 67
catgcatcaa acaccgctac aagcgacgacg atcgtcgaa gcataaaagtgc gcctgc   56

<210> 68
<211> 56
<212> DNA
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<220>
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<400> 68
ctaggcaggc cactttatgc ttccgacgat cgcgatcgctt gtatcggtgt ttgatg      56

<210> 69
<211> 56
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<400> 69
catgcatcaa acaccgctac aagcgacgacg atcgtcgaa gcataaaagtgc gcctgc   56

<210> 70
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peptide

<400> 70
Ala Cys Ile Lys His Arg Tyr Lys Arg Arg Asp Arg Arg Lys His Lys
1 5 10 15
Val Ala Cys Ile Gly
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<210> 71
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
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<400> 71
ctaggcaggc cacttatgc ttccgacgt cgcgtcgctt gtgcggtgt ttgatg 56

<210> 72
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
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<400> 72
attatcctag gtcaaatggc agtattcatc cac 33

<210> 73
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
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<400> 73
tataggatcc taatcctcat cctgtctact tgc 33

<210> 74
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
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<400> 74
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33

<210> 75
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 caaatggcag tattcatcca caatttaaa agaaaagggg ggattgggg gtacagtgc 60
 ggggaaagaa tagtagacat aatagcaaca gacataaaaa ctaaagaatt acaaaaacaa 120
 attacaaaaaa ttcaaaaattt tcgggttat tacagggaca gcagaaatcc actttggaaa 180
 ggaccaggcaa agtcctctg gaaaggtgaa ggggcagtag taatacaaga taatagtgc 240
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 peptide

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 Cys Ile Gly Gln Met Ala Val Phe Ile His Asn Phe Lys Arg Lys Gly
 1 5 10 15
 Gly Ile Gly Gly Tyr Ser Ala Gly Glu Arg Ile Val Asp Ile Ile Ala
 20 25 30
 Thr Asp Ile Gln Thr Lys Glu Leu Gln Lys Ile Thr Lys Ile Gln
 35 40 45
 Asn Phe Arg Val Tyr Tyr Asp Ser Arg Asn Pro Leu Trp Lys Gly
 50 55 60
 Pro Ala Lys Leu Leu Trp Lys Gly Glu Gly Ala Val Val Ile Gln Asp
 65 70 75 80
 Asn Ser Asp Ile Lys Val Val Pro Arg Arg Lys Ala Lys Ile Ile Arg
 85 90 95
 Asp Tyr Gly Lys Gln Met Ala Gly Asp Asp Cys Val Ala Ser Arg Gln
 100 105 110

Asp Glu Asp
115

<210> 77
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tataggatcc taatcctcat cctgtctact tgc 33

<210> 78
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catatgttt tagatggaat agataaggcc caagatgaac atgagaaaata tcacagtaat 60
tggagagcaa tggctagtga tttaaacctg ccacctggc ccaaaaaggc ccgtcgcatc 120
aagggcaaaa tgccacgggt gaagaaagcc ggcgttagtag caaaaagaaaat agtagccagc 180
tgtgataaat gtcagctaaa aggagaagcc atgcattggac aagtagactg tagtccagga 240
atatggcaac tagattgtac acattttagaa ggaaaagttt tcctggtagc agttcatgt 300
gccagtggat atatagaagc agaagtattt ccagcagaaa cagggcagga aacagcatat 360
ggagccatgca tcaaaccaccc ctacaaggcga cgccatcgatc ggaagcataa agtggccatgc 420
ctaggtcaaa tggcagtatt catccacaat tttaaaagaa aaggggggat tgggggggtac 480
agtgcagggg aaagaataagt agacataata gcaacagaca tacaaactaa agaattacaa 540
aaacaaatata caaaaattca aaattttcgg gtttattaca gggacagcag aaatccactt 600
tgaaaaggac cagcaaagct cctctggaaa ggtgaagggg cagtagtaat acaagataat 660
agtgcacataa aagttagtgcc aagaagaaaa gcaaagatca ttagggatta tgaaaacag 720
atggcagggt atgattgtgt ggcaagtaga caggatgagg attaggatcc 770

<210> 79
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 79
Met Phe Leu Asp Gly Ile Asp Lys Ala Gln Asp Glu His Glu Lys Tyr
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His Ser Asn Trp Arg Ala Met Ala Ser Asp Phe Asn Leu Pro Pro Gly
20 25 30

Pro Lys Lys Ala Arg Arg Ile Lys Gly Lys Met Arg Arg Val Lys Lys
 35 40 45

Ala Gly Val Val Ala Lys Glu Ile Val Ala Ser Cys Asp Lys Cys Gln
 50 55 60

Leu Lys Gly Glu Ala Met His Gly Gln Val Asp Cys Ser Pro Gly Ile
 65 70 75 80

Trp Gln Leu Asp Cys Thr His Leu Glu Gly Lys Val Ile Leu Val Ala
 85 90 95

Val His Val Ala Ser Gly Tyr Ile Glu Ala Glu Val Ile Pro Ala Glu
 100 105 110

Thr Gly Gln Glu Thr Ala Tyr Gly Ala Cys Ile Lys His Arg Tyr Lys
 115 120 125

Arg Arg Asp Arg Arg Lys His Lys Val Ala Cys Ile Gly Gln Met Ala
 130 135 140

Val Phe Ile His Asn Phe Lys Arg Lys Gly Gly Ile Gly Gly Tyr Ser
 145 150 155 160

Ala Gly Glu Arg Ile Val Asp Ile Ile Ala Thr Asp Ile Gln Thr Lys
 165 170 175

Glu Leu Gln Lys Gln Ile Thr Lys Ile Gln Asn Phe Arg Val Tyr Tyr
 180 185 190

Arg Asp Ser Arg Asn Pro Leu Trp Lys Gly Pro Ala Lys Leu Leu Trp
 195 200 205

Lys Gly Glu Gly Ala Val Val Ile Gln Asp Asn Ser Asp Ile Lys Val
 210 215 220

Val Pro Arg Arg Lys Ala Lys Ile Ile Arg Asp Tyr Gly Lys Gln Met
 225 230 235 240

Ala Gly Asp Asp Cys Val Ala Ser Arg Gln Asp Glu Asp
 245 250

<210> 80

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
6X His tag

<400> 80

His His His His His His

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<210> 81

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 81

Met	Gly	Ser	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr
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Lys	Val	Val	Lys	Ile	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Lys	Ala	Lys
					20				25				30		

Arg	Arg	Val	Val	Gln	Arg	Glu	Lys	Arg	Ala	Val	Gly	Ile	Gly	Ser	Arg
					35			40				45			

Gln	Leu	Leu	Ser	Gly	Ile	Val	Gln	Gln	Asn	Asn	Leu	Leu	Arg	Ala	
					50		55				60				

Ile	Glu	Ala	Gln	Gln	His	Leu	Leu	Gln	Leu	Thr	Val	Trp	Gly	Ile	Lys
	65					70				75			80		

Gln	Leu	Leu	Arg	Ile	Leu	Ala	Val	Glu	Arg	Tyr	Leu	Lys	Asp	Gln	
			85					90				95			

Gln	Leu	Leu	Gly	Ile	Trp	Gly	Cys	Ser	Gly	Lys	Leu	Ile	Cys	Thr	Thr
			100					105				110			

Ala	Val	Pro	Trp	Asn	Ala	Ser	Trp	Ser	Asn	Lys	Ser	Leu	Glu	Gln	Ile
				115			120				125				

Trp	Asn	Asn	Met	Thr	Trp	Met	Glu	Trp	Asp	Arg	Glu	Ile	Asn	Asn	Tyr
			130			135				140					

Thr	Ser	Leu	Ile	His	Ser	Leu	Ile	Glu	Glu	Ser	Gln	Asn	Gln	Gln	Glu
	145					150			155			160			

Lys	Asn	Glu	Gln	Glu	Leu	Leu	Glu	Leu	Asp	Lys	Trp	Ala	Ser	Leu	Trp
			165					170			175				

Asn	Trp	Phe	Asn	Ile	Thr	Asn	Trp	Leu	Ala	Met	Glu	Lys	Tyr	Leu	Lys
			180				185				190				

Asp	Gln	Ala	Arg	Leu	Asn	Ser	Trp	Gly	Cys	Ala	Phe	Arg	Gln	Val	Cys
			195				200				205				

His	Asp	Arg	Pro	Glu	Gly	Ile	Glu	Glu	Gly	Gly	Glu	Arg	Asp	Arg	
			210				215				220				

Asp	Arg	Ser	Ile	Arg	Leu	Val	Asn								
	225				230										

<210> 82

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 82

Met	Gly	Ser	Asp	Met	Arg	Asp	Asn	Trp	Ile	Gln	Asn	Gln	Gln	Leu	Leu
1				5					10					15	
Asn	Leu	Trp	Gly	Cys	Lys	Gly	Arg	Leu	Val	Cys	Tyr	Thr	Asn	Trp	Arg
				20				25					30		
Ser	Glu	Leu	Tyr	Lys	Tyr	Lys	Val	Val	Lys	Ile	Glu	Pro	Leu	Gly	Val
				35			40			45					
Ala	Pro	Thr	Lys	Ala	Lys	Arg	Arg	Val	Val	Gln	Arg	Glu	Lys	Arg	Ala
				50			55			60					
Val	Gly	Ile	Gly	Ser	Arg	Gln	Leu	Leu	Ser	Gly	Ile	Val	Gln	Gln	Gln
				65			70			75			80		
Asn	Asn	Leu	Leu	Arg	Ala	Ile	Glu	Ala	Gln	Gln	His	Leu	Leu	Gln	Leu
				85				90			95				
Thr	Val	Trp	Gly	Ile	Lys	Gln	Leu	Gln	Ala	Arg	Ile	Leu	Ala	Val	Glu
				100			105			110					
Arg	Tyr	Leu	Lys	Asp	Gln	Gln	Leu	Leu	Gly	Ile	Trp	Gly	Cys	Ser	Gly
				115			120			125					
Lys	Leu	Ile	Cys	Thr	Thr	Ala	Val	Pro	Trp	Asn	Ala	Ser	Trp	Ser	Asn
				130			135			140					
Lys	Ser	Leu	Glu	Gln	Ile	Trp	Asn	Asn	Met	Thr	Trp	Met	Glu	Trp	Asp
				145			150			155			160		
Arg	Glu	Ile	Asn	Asn	Tyr	Thr	Ser	Leu	Ile	His	Ser	Leu	Ile	Glu	Glu
				165				170			175				
Ser	Gln	Asn	Gln	Gln	Glu	Lys	Asn	Glu	Gln	Glu	Leu	Leu	Glu	Leu	Asp
				180				185			190				
Lys	Trp	Ala	Ser	Leu	Trp	Asn	Trp	Phe	Asn	Ile	Thr	Asn	Trp	Leu	Ala
				195			200			205					
Met	Glu	Lys	Tyr	Leu	Lys	Asp	Gln	Ala	Arg	Leu	Asn	Ser	Trp	Gly	Cys
				210			215			220					
Ala	Phe	Arg	Gln	Val	Cys	His	Asp	Arg	Pro	Glu	Gly	Ile	Glu	Glu	Glu
				225			230			235			240		
Gly	Gly	Glu	Arg	Asp	Arg	Asp	Arg	Ser	Ile	Arg	Leu	Val	Asn		
				245				250							

<210> 83

<211> 297

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 83

Met	Gly	Lys	Arg	Ala	His	Lys	Ser	Arg	Lys	Ile	Lys	Arg	Val	Thr	Arg
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Arg	Gly	Ala	Val	Gly	Ile	Gly	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Asn	Asn
															30
20								25							

Thr	Arg	Lys	Ser	Val	Arg	Ile	Gly	Pro	Gly	Gln	Ala	Phe	Tyr	Ala	Thr
															45
35							40								

Gly	Asp	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Ile	Gly	Pro
															60
50						55									

Thr	Pro	Thr	Gly	Trp	Lys	Lys	Asn	Arg	Arg	Leu	Lys	Gly	Lys	Tyr	Arg
															80
65							70			75					

Arg	Met	Lys	Lys	Trp	Gly	Ala	Val	Gly	Ile	Gly	Ile	Asn	Cys	Thr	Arg
															95
85								90							

Pro	Asn	Asn	Asn	His	Thr	Arg	Lys	Ser	Ile	His	Ile	Gly	Pro	Gly	Arg
															110
100								105							

Ala	Phe	Tyr	Ala	Thr	Ser	Gly	Asp	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala
															125
115						120									

His	Cys	Asn	Ile	Gly	Pro	Thr	Pro	Thr	Gly	Ala	Cys	Val	Lys	His	Arg
															140
130							135								

Gln	Lys	Arg	Lys	Glu	Lys	Arg	Lys	Tyr	Lys	Thr	Ala	Cys	Val	Gly	Ala
															160
145				150					155						

Val	Gly	Ile	Gly	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Asn	Thr	Arg	Lys
														175
165							170							

Ser	Ile	His	Leu	Gly	Pro	Gly	Gln	Ala	Phe	Tyr	Ala	Thr	Gly	Asp	Gly
															190
180							185								

Asp	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Ile	Gly	Pro	Thr
															205
195						200									

Pro	Thr	Gly	Ser	Lys	Lys	Ala	Arg	Arg	Ile	Lys	Gly	Lys	Met	Arg	Arg
															220
210							215								

Leu	Lys	Lys	Val	Gly	Ala	Val	Gly	Ile	Gly	Ile	Asn	Cys	Thr	Arg	Pro
															240
225							230				235				

Asn	Asn	Asn	Gly	His	Thr	Arg	Lys	Ser	Ile	Arg	Ile	Gly	Pro	Gly	Gln
															255
245								250							

Thr Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His
260 265 270

Cys Asn Ile Gly Pro Thr Pro Thr Gly Lys Arg Ala Val Lys Ser Arg
275 280 285

Lys Tyr Lys Arg His Ile Arg Arg Gly
290 295

<210> 84
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 84
Met Gly Ser Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr
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Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys
20 25 30

Arg Arg Val Val Gln Arg Glu Ala Leu Glu Thr Leu Leu Gln Asn Gln
35 40 45

Gln Ile Leu Asn Leu Trp Gly Cys Lys Gly Arg Leu Ile Cys Tyr Trp
50 55 60

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Leu
65 70 75 80

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
 85 90 95

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
 100 105 110

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
115 120 125

Asn	Asn	Tyr	Thr	Ser	Leu	Ile	His	Ser	Leu	Ile	Glu	Glu	Ser	Gln	Asn
130					135						140				

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
145 150 155 160

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Ala Ile Glu Lys
165 170 175

Tyr Leu Lys Asp Gln Ala Arg Leu Asn Ser Trp Gly Cys Ala Phe Arg
 180 185 190

Gln Val Cys His Asp Arg Pro Glu Gly Ile Glu Glu Glu Gly Gly Glu
195 200 205

Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
 210 215 220

<210> 85
 <211> 500
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 85
 Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
 1 5 10 15
 Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
 20 25 30
 His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
 35 40 45
 Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
 50 55 60
 Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
 65 70 75 80
 Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
 85 90 95
 Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Gln Asn Lys Ser Lys
 100 105 110
 Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn Gln Val
 115 120 125
 Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
 130 135 140
 Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
 145 150 155 160
 Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
 165 170 175
 Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
 180 185 190
 Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
 195 200 205
 Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
 210 215 220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
 225 230 235 240

 Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
 245 250 255

 Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
 260 265 270

 Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
 275 280 285

 Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
 290 295 300

 Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
 305 310 315 320

 Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
 325 330 335

 Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
 340 345 350

 Val Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser
 355 360 365

 Gln Val Thr Asn Ser Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg
 370 375 380

 Asn Gln Arg Lys Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His
 385 390 395 400

 Thr Ala Arg Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys
 405 410 415

 Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn
 420 425 430

 Phe Leu Gly Lys Ile Trp Pro Ser Tyr Lys Gly Arg Pro Gly Asn Phe
 435 440 445

 Leu Gln Ser Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser Phe Arg
 450 455 460

 Ser Gly Val Glu Thr Thr Pro Pro Gln Lys Gln Glu Pro Ile Asp
 465 470 475 480

 Lys Glu Leu Tyr Pro Leu Thr Ser Leu Arg Ser Leu Phe Gly Asn Asp
 485 490 495

 Pro Ser Ser Gln
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<210> 86
 <211> 696

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<212> PRT
<213> Artificial Sequence

<220>
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      peptide

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<223> Asp or Glu

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<223> Any amino acid

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<223> This molecule may encompass smaller embodiments according
      to the application as filed.

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Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
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Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Tyr Lys Leu Lys
     20          25           30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
     35          40           45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
     50          55           60

Gln Pro Ser Leu Gln Thr Ser Glu Glu Leu Arg Ser Leu Tyr Asn
     65          70           75          80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
     85           90          95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Gln Asn Lys Ser Lys
    100          105          110

Lys Lys Ala Gln Gln Ala Ala Asp Thr Gly His Ser Asn Gln Val
    115          120          125

Ser Gln Asn Tyr Gly Lys Arg Xaa Xaa Lys Xaa Arg Lys Xaa Lys Arg
    130          135          140

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Xaa Xaa Arg Arg Gly Gly Xaa Cys Xaa Lys Xaa Arg Xaa Lys Arg Arg
 145 150 155 160
 Xaa Arg Arg Lys Xaa Lys Xaa Xaa Cys Xaa Gly Pro Ile Val Gln Asn
 165 170 175
 Ile Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn
 180 185 190
 Ala Trp Val Lys Val Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile
 195 200 205
 Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn
 210 215 220
 Thr Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met Gln Met Leu
 225 230 235 240
 Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro
 245 250 255
 Val His Ala Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly
 260 265 270
 Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp
 275 280 285
 Gly Xaa Lys Lys Xaa Arg Arg Xaa Lys Gly Lys Xaa Arg Arg Xaa Lys
 290 295 300
 Lys Xaa Gly Gly Xaa Cys Xaa Lys Xaa Arg Xaa Lys Arg Arg Xaa Arg
 305 310 315 320
 Arg Lys Xaa Lys Xaa Xaa Cys Xaa Gly Met Thr Asn Asn Pro Pro Ile
 325 330 335
 Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
 340 345 350
 Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
 355 360 365
 Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
 370 375 380
 Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
 385 390 395 400
 Leu Leu Val Gly Lys Arg Xaa Xaa Lys Xaa Arg Lys Xaa Lys Arg Xaa
 405 410 415
 Xaa Arg Arg Gly Gly Xaa Lys Lys Xaa Arg Arg Xaa Lys Gly Lys Xaa
 420 425 430
 Arg Arg Xaa Lys Lys Xaa Gly Gly Xaa Cys Xaa Lys Xaa Arg Xaa Lys
 435 440 445

Arg Arg Xaa Arg Arg Lys Xaa Lys Xaa Xaa Cys Xaa Gly Gln Asn Ala
 450 455 460
 Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr
 465 470 475 480
 Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His
 485 490 495
 Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Val Thr Asn Ser Ala
 500 505 510
 Thr Ile Met Met Gln Arg Gly Asn Phe Arg Asn Gln Arg Lys Ile Val
 515 520 525
 Lys Cys Phe Asn Cys Gly Lys Glu Gly His Thr Ala Arg Asn Cys Arg
 530 535 540
 Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly His Gln
 545 550 555 560
 Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys Ile Trp
 565 570 575
 Pro Ser Tyr Lys Gly Arg Pro Gly Asn Phe Leu Gln Gly Lys Arg Xaa
 580 585 590
 Xaa Lys Xaa Arg Lys Xaa Lys Arg Xaa Xaa Arg Arg Gly Gly Xaa Lys
 595 600 605
 Lys Xaa Arg Arg Xaa Lys Gly Lys Xaa Arg Arg Xaa Lys Lys Xaa Gly
 610 615 620
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 Glu Ser Phe Arg Ser Gly Val Glu Thr Thr Pro Pro Gln Lys Gln
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 Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile
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 His Pro Ala Gly Leu Lys Lys Ser Val Thr Val Leu Asp Val
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 Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr
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 245 250 255
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Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr
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 325 330 335
 Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr
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 Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys Gln
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 Leu Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile Trp
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 Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala Asn
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Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile
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Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Gly Lys Arg
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Xaa Xaa Lys Xaa Arg Lys Xaa Lys Arg Xaa Xaa Arg Arg Gly Gly Xaa
 65 70 80

Lys Lys Xaa Arg Arg Xaa Lys Gly Lys Xaa Arg Arg Xaa Lys Lys Xaa
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Gly Gly Xaa Cys Xaa Lys Xaa Arg Xaa Lys Arg Arg Xaa Arg Arg Lys
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Xaa Lys Xaa Xaa Cys Xaa Gly Phe Ala Ile Lys Lys Asp Ser Thr
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Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln
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Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys
 145 150 155 160

Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser
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Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro
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Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu
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Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr
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Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro Asn Ile Val Ile Tyr
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Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln
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His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly
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Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Gly Lys
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 355 360 365
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 Ser Gln Ile Tyr Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu
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 Glu Ala Met His Gly Gln Val Asp Cys Ser Pro Gly Ile Trp Gln Leu
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 Asp Cys Thr His Leu Glu Gly Lys Val Ile Leu Val Ala Val His Val
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 Ala Ser Gly Tyr Ile Glu Ala Glu Val Ile Pro Ala Glu Thr Gly Gln
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85 90 95Ala Ser Cys Asp Lys Cys Gln Leu Lys Gly Glu Ala Met His Gly Gln
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115 120 125Gly Lys Val Ile Leu Val Ala Val His Val Ala Ser Gly Tyr Ile Glu
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Arg Xaa Xaa Lys Xaa Arg Lys Xaa Lys Arg Xaa Xaa Arg Arg Gly Gly
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 Trp Pro Val Lys Thr Ile His Thr Asp Asn Gly Ser Asn Phe Thr Ser
 225 230 235 240
 Ala Thr Val Lys Ala Ala Cys Trp Trp Ala Gly Ile Lys Gln Glu Phe
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 Ile Gly Gln Val Arg Asp Gln Ala Glu His Leu Lys Thr Ala Val Gly
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 Gln Ile Thr Lys Ile Gln Asn Phe Arg Val Tyr Tyr Arg Asp Ser Arg
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Asn Pro Leu Trp Lys Gly Pro Ala Lys Leu Leu Trp Lys Gly Glu Gly
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Ala Val Val Ile Gln Asp Asn Ser Asp Ile Lys Val Val Pro Arg Arg
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Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val Val Leu Val Asn
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Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asp Met Val Glu Gln Met
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His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val
 85 90 95

Lys Leu Thr Pro Leu Cys Val Ser Leu Lys Glu Cys Thr Asp Leu Lys
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Asp Asn Asp Thr Thr Ser Tyr Lys Leu Thr Ser Cys Asn Thr Ser Val
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 Glu Gly Ser Asp Leu Gln Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln
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 Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr
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Ile	His	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Thr	Ser	Thr	Arg	Lys
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Ser	Ile	His	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Thr	Ser	Met	Gln
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Gln	Thr	Arg	Thr	Ser	Ile	Thr	Ile	Gly	Pro	Gly	Gln	Val	Phe	Tyr	Arg
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Tyr	Ala	Thr	Gly	Thr	Arg	Lys	Gly	Ile	His	Ile	Gly	Pro	Gly	Arg	Ala
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Phe	Tyr	Ala	Thr	Gly	Ser	His	Gly	Thr	Glu	Lys	Leu	Trp	Val	Thr	Val
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Tyr	Tyr	Gly	Val	Pro	Val	Trp	Lys	Glu	Ala	Thr	Thr	Leu	Phe	Cys	
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Val Ser Leu Lys Glu Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn
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 Tyr Thr Thr Lys Ile Glu Thr Arg Lys Ser Ile His Leu Gly Pro Gly
 1620 1625 1630
 Gln Ala Phe Tyr Ala Thr Gly Asp Tyr Gln Thr Arg Lys Ser Ile Arg
 1635 1640 1645
 Ile Gly Pro Gly Gln Ala Phe Tyr Ala Thr Gly Asp Thr Val Gln Glu
 1650 1655 1660
 Ile Arg Ile Gly Pro Met Ala Trp Tyr Ser Met Gly Asn Val Thr Arg
 1665 1670 1675 1680
 Ile Ser His Thr Ile Gly Pro Gly Arg Val Phe Tyr Arg Thr Thr Arg
 1685 1690 1695
 Lys Gly Ile His Met Gly Pro Gly Gln Val Leu Tyr Ala Thr Lys Pro
 1700 1705 1710
 His Thr Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Ala
 1715 1720 1725
 Thr Ser Thr Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr
 1730 1735 1740
 Thr Thr Ser Met Gln Gln Thr Arg Thr Ser Ile Thr Ile Gly Pro Gly
 1745 1750 1755 1760
 Gln Val Phe Tyr Arg Thr Glu Gly Thr Arg Lys Ser Val Arg Ile Gly
 1765 1770 1775
 Pro Gly Gln Thr Phe Tyr Ala Thr Gly Thr Arg Lys Gly Ile His Ile
 1780 1785 1790
 Gly Pro Gly Arg Ala Phe Tyr Ala Thr Gly Gly Pro Cys Thr Asn Val
 1795 1800 1805

Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln
 1810 1815 1820

Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser
 1825 1830 1835 1840

Val Gly Lys Arg Xaa Xaa Lys Xaa Arg Lys Xaa Lys Arg Xaa Xaa Arg
 1845 1850 1855

Arg Gly Gly Xaa Lys Xaa Arg Arg Xaa Lys Gly Lys Xaa Arg Arg
 1860 1865 1870

Xaa Lys Lys Xaa Gly Gly Xaa Cys Xaa Lys Xaa Arg Xaa Lys Arg Arg
 1875 1880 1885

Xaa Arg Arg Lys Xaa Lys Xaa Xaa Cys Xaa Gly Asn Phe Thr Asp Asn
 1890 1895 1900

Ala Lys Thr Ile Ile Val Gln Leu Asn Thr Ser Val Glu Ile Asn Cys
 1905 1910 1915 1920

Thr Arg Pro Asn Asn Asn Thr Arg Lys Arg Ile Arg Ile Gln Arg Gly
 1925 1930 1935

Pro Gly Arg Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln
 1940 1945 1950

Ala His Cys Asn Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Lys Gln
 1955 1960 1965

Ile Ala Ser Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile
 1970 1975 1980

Phe Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe
 1985 1990 1995 2000

Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn
 2005 2010 2015

Ser Thr Trp Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr
 2020 2025 2030

Glu Gly Ser Asp Leu Gln Thr Arg Lys Ser Ile His Ile Gly Pro Gly
 2035 2040 2045

Gln Ala Phe Tyr Ala Thr Gly Asp Thr Arg Arg Ser Ile Ser Phe Gly
 2050 2055 2060

Ile Gly Pro Gly Gln Ala Leu Tyr Thr Thr Arg Gln Arg Thr Pro
 2065 2070 2075 2080

Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr Gly Gln Phe Arg Thr Val
 2085 2090 2095

Gln Glu Ile Arg Ile Gly Pro Met Ala Trp Tyr Ser Met Gly Ala Thr
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Met Lys Arg Thr Ser Ile His Ile Gly Pro Gly Gln Thr Phe Tyr Ala
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 Thr Thr Arg Arg Gly Ile Pro Leu Gly Pro Gly Arg Ala Trp Tyr Ala
 2130 2135 2140

 Thr Leu Asp Ser Thr Arg Glu Ser Met Arg Ile Gly Pro Gly Gln Ala
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 Phe Tyr Ala Thr Gly Ile Arg Gln Gly Ile His Ile Gly Pro Gly Arg
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 Ala Phe Phe Ala Ala Trp Asp Val Gln Glu Met Arg Ile Gly Pro Met
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 Ala Trp Tyr Ser Met Gly Ile Cys Thr Arg Arg Gly Ile Arg Met Gly
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 Pro Gly Gln Val Val Tyr Ala Thr Cys Thr Thr Ile Val Gln Ile Lys
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 Ile Ile Gly Pro Leu Ala Val Tyr Ser Met Tyr Gly Thr Arg Lys Ser
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 Val Arg Ile Gly Pro Gly Gln Ala Phe Tyr Ala Thr Gly His Thr Arg
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 Lys Ser Ile Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Asn Thr
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 Arg Gln Ser Thr His Ile Gly Pro Gly Ala Leu Tyr Thr Thr Lys Ile
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 Glu Thr Arg Lys Ser Ile His Leu Gly Pro Gly Gln Ala Phe Tyr Ala
 2290 2295 2300

 Thr Gly Asp Tyr Gln Thr Arg Lys Ser Ile Arg Ile Gly Pro Gly Gln
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 Ala Phe Tyr Ala Thr Gly Asp Thr Val Gln Glu Ile Arg Ile Gly Pro
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 Met Ala Trp Tyr Ser Met Gly Asn Val Thr Arg Ile Ser His Thr Ile
 2340 2345 2350

 Gly Pro Gly Arg Val Phe Tyr Arg Thr Thr Arg Lys Gly Ile His Met
 2355 2360 2365

 Gly Pro Gly Gln Val Leu Tyr Ala Thr Lys Pro His Thr Arg Lys Ser
 2370 2375 2380

 Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Thr Ser Thr Arg Lys
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 Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Ser Met Gln
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Gln Thr Arg Thr Ser Ile Thr Ile Gly Pro Gly Gln Val Phe Tyr Arg
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Thr Glu Gly Thr Arg Lys Ser Val Arg Ile Gly Pro Gly Gln Thr Phe
 2435 2440 2445

Tyr Ala Thr Gly Thr Arg Lys Gly Ile His Ile Gly Pro Gly Arg Ala
 2450 2455 2460

Phe Tyr Ala Thr Gly Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile
 2465 2470 2475 2480

Ile Asn Met Trp Gln Lys Val Gly Lys Ala Met Tyr Ala Pro Gly Lys
 2485 2490 2495

Arg Xaa Xaa Lys Xaa Arg Lys Xaa Lys Arg Xaa Xaa Arg Arg Gly Gly
 2500 2505 2510

Xaa Lys Lys Xaa Arg Arg Xaa Lys Gly Lys Xaa Arg Arg Xaa Lys Lys
 2515 2520 2525

Xaa Gly Gly Xaa Cys Xaa Lys Xaa Arg Xaa Lys Arg Arg Xaa Arg Arg
 2530 2535 2540

Lys Xaa Lys Xaa Xaa Cys Xaa Gly Pro Ile Ser Gly Gln Ile Arg Cys
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Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser
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Asn Asn Glu Ser Glu Ile Phe Arg Pro Gly Gly Asp Ser Thr Arg Glu
 2580 2585 2590

Ser Met Arg Ile Gly Pro Gly Gln Ala Phe Tyr Ala Thr Gly Asp Val
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Gln Glu Met Arg Ile Gly Pro Met Ala Trp Tyr Ser Met Gly Gln Thr
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Arg Thr Ser Ile Thr Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Glu
 2625 2630 2635 2640

Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val
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				20					25					30			
Arg Arg Val Val Gln Arg Glu Lys Arg Ala Val Gly Ile Gly Ser Ala																	
				35					40					45			
Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala																	
				50					55					60			
Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val																	
				65					70					75			80
Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu																	
				85					90					95			
Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu																	
				100					105					110			
Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly																	
				115					120					125			
Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser																	
				130					135					140			
Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn Asn Met Thr Trp Met																	
				145					150					155			160
Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu																	
				165					170					175			
Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu																	
				180					185					190			
Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn																	
				195					200					205			
Trp Leu Glu Phe Asn Asn Trp Tyr Ile Lys Leu Phe Ile Met Ile Val																	
				210					215					220			
Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Ile Val																	
				225					230					235			240
Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His Leu																	
				245					250					255			
Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Gly																	
				260					265					270			
Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser Leu																	
				275					280					285			

Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His
290 295 300

Arg Leu Arg Asp Leu Leu Ile Val Thr Arg Ile Val Glu Leu Leu
305 310 315 320

Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu Gln
325 330 335

Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn Ala
340 345 350

Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val Val
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Gln Gly Ala Cys Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg Gln
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Gly Leu Glu Arg Ile Leu Leu
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      to the application as filed.

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Lys Xaa Lys Arg Xaa Xaa Arg Arg Gly Gly Xaa Lys Lys Xaa Arg Arg
    20          25          30

Xaa Lys Gly Lys Xaa Arg Arg Xaa Lys Lys Xaa Gly Trp Ile Gln Leu
    35          40          45

Gln Gln Arg Leu Asn Leu Trp Gly Cys Arg Gly Lys Leu Ile Cys Tyr
    50          55          60

Thr Asn Trp Ile Gln Asn Gln Gln Leu Leu Asn Leu Trp Gly Cys Lys
    65          70          75          80

Gly Arg Leu Val Cys Tyr Thr Asn Trp Leu Gln Asn Gln Gln Ile Leu
    85          90          95

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Asn Leu Trp Gly Cys Lys Gly Arg Leu Ile Cys Tyr Thr Asn Trp Leu
 100 105 110
 Gln Ser Gln Gln Leu Leu Ser Asn Trp Gly Cys Arg Gly Lys Leu Val
 115 120 125
 Cys Tyr Thr Asn Ala Ile Glu Arg Tyr Leu Gln Asp Gln Ala Arg Leu
 130 135 140
 Asn Ser Trp Gly Cys Thr Phe Arg Gln Val Cys His Ala Met Glu Lys
 145 150 155 160
 Tyr Leu Lys Asp Gln Ala Arg Leu Asn Ser Trp Gly Cys Ala Phe Arg
 165 170 175
 Gln Val Cys His Ala Ile Glu Lys Tyr Leu Lys His Gln Ala Gln Leu
 180 185 190
 Asn Ala Trp Gly Cys Ala Phe Arg Gln Val Cys His Trp Arg Ser Glu
 195 200 205
 Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro
 210 215 220
 Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala Val Gly
 225 230 235 240
 Ile Gly Ser Ala Ile Glu Arg Tyr Leu Gln Asp Gln Ala Arg Leu Asn
 245 250 255
 Ser Trp Gly Cys Thr Phe Arg Gln Val Cys His Ala Met Glu Lys Tyr
 260 265 270
 Leu Arg Asp Gln Ala Ile Val Asn Ser Trp Gly Cys Ala Phe Arg Gln
 275 280 285
 Val Cys Tyr Ala Met Glu Lys Tyr Leu Lys Asp Gln Ala Arg Leu Asn
 290 295 300
 Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His Ala Leu Phe Leu Gly
 305 310 315 320
 Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Met Thr Leu
 325 330 335
 Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn
 340 345 350
 Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr
 355 360 365
 Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Gly Lys Arg Xaa
 370 375 380
 Xaa Lys Xaa Arg Lys Xaa Lys Arg Xaa Xaa Arg Arg Gly Gly Xaa Lys
 385 390 395 400

Lys Xaa Arg Arg Xaa Lys Gly Lys Xaa Arg Arg Xaa Lys Lys Xaa Gly
 405 410 415
 Gly Xaa Cys Xaa Lys Xaa Arg Xaa Lys Arg Arg Xaa Arg Arg Lys Xaa
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 Lys Xaa Xaa Cys Xaa Gly Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln
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 Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala
 450 455 460
 Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp
 465 470 475 480
 Asn Asn Met Thr Trp Met Glu Trp Ile Gln Leu Gln Gln Arg Leu Asn
 485 490 495
 Leu Trp Gly Cys Arg Gly Lys Leu Ile Cys Tyr Thr Asn Trp Leu Gln
 500 505 510
 Asn Gln Gln Ile Leu Asn Leu Trp Gly Cys Lys Gly Arg Leu Ile Cys
 515 520 525
 Tyr Thr Asn Trp Leu Gln Ser Gln Gln Leu Leu Ser Asn Trp Gly Cys
 530 535 540
 Arg Gly Lys Leu Val Cys Tyr Thr Asn Trp Asp Arg Glu Ile Asn Asn
 545 550 555 560
 Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln
 565 570 575
 Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu
 580 585 590
 Trp Asn Trp Ile Gln Asn Gln Gln Leu Leu Asn Leu Trp Gly Cys Lys
 595 600 605
 Gly Arg Leu Val Cys Tyr Thr Asn Trp Leu Gln Asn Gln Ile Leu
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 Asn Leu Trp Gly Cys Lys Gly Arg Leu Ile Cys Tyr Thr Asn Trp Phe
 625 630 635 640
 Asn Ile Thr Asn Trp Leu Glu Phe Asn Asn Trp Ile Gln Asn Gln Gln
 645 650 655
 Leu Leu Asn Leu Trp Gly Cys Lys Gly Arg Leu Val Cys Tyr Thr Asn
 660 665 670
 Trp Leu Gln Asn Gln Gln Ile Leu Asn Leu Trp Gly Cys Lys Gly Arg
 675 680 685
 Leu Ile Cys Tyr Thr Asn Trp Leu Gln Ser Gln Gln Leu Leu Ser Asn
 690 695 700

Trp Gly Cys Arg Gly Lys Leu Val Cys Tyr Thr Asn Trp Gly Lys Arg
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Xaa Xaa Lys Xaa Arg Lys Xaa Lys Arg Xaa Xaa Arg Arg Gly Gly Xaa
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Lys Lys Xaa Arg Arg Xaa Lys Gly Lys Xaa Arg Arg Xaa Lys Lys Xaa
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Gly Gly Xaa Cys Xaa Lys Xaa Arg Xaa Lys Arg Arg Xaa Arg Arg Lys
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Xaa Lys Xaa Xaa Cys Xaa Gly Ala Ile Glu Arg Tyr Leu Gln Asp Gln
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Ala Arg Leu Asn Ser Trp Gly Cys Thr Phe Arg Gln Val Cys His Ala
 785 790 795 800

Met Glu Lys Tyr Leu Arg Asp Gln Ala Ile Val Asn Ser Trp Gly Cys
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Ala Phe Arg Gln Val Cys Tyr Ala Met Glu Lys Tyr Leu Lys Asp Gln
 820 825 830

Ala Arg Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His Ala
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Ile Glu Lys Tyr Leu Lys His Gln Ala Gln Leu Asn Ala Trp Gly Cys
 850 855 860

Ala Phe Arg Gln Val Cys His Trp Tyr Ile Lys Leu Phe Ile Met Ile
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Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Ile
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Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
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Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
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Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Ala Met
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Glu Lys Tyr Leu Arg Asp Gln Ala Ile Val Asn Ser Trp Gly Cys Ala
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Phe Arg Gln Val Cys Tyr Ala Met Glu Lys Tyr Leu Lys Asp Gln Ala
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Arg Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His Gly Ser
 980 985 990

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
 995 1000 1005

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
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 Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
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 Gln Tyr Trp Ser Gln Glu Leu Lys Gly Lys Arg Xaa Xaa Lys Xaa Arg
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 Lys Xaa Lys Arg Xaa Xaa Arg Arg Gly Gly Xaa Cys Xaa Lys Xaa Arg
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 Xaa Lys Arg Arg Xaa Arg Arg Lys Xaa Lys Xaa Cys Xaa Gly Ala
 1075 1080 1085

 Ile Glu Arg Tyr Leu Gln Asp Gln Ala Arg Leu Asn Ser Trp Gly Cys
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 Thr Phe Arg Gln Val Cys His Ala Met Glu Lys Tyr Leu Arg Asp Gln
 1105 1110 1115 1120

 Ala Ile Val Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys Tyr Ala
 1125 1130 1135

 Met Glu Lys Tyr Leu Lys Asp Gln Ala Arg Leu Asn Ser Trp Gly Cys
 1140 1145 1150

 Ala Phe Arg Gln Val Cys His Ala Ile Glu Lys Tyr Leu Lys His Gln
 1155 1160 1165

 Ala Gln Leu Asn Ala Trp Gly Cys Ala Phe Arg Gln Val Cys His Asn
 1170 1175 1180

 Ser Ala Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly
 1185 1190 1195 1200

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 His Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
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 peptide

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Ser Leu Thr Val Ser Ala Gln Ser Arg Thr Leu Leu Ala Gly Ile Val
 35 40 45

 Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg Gln Gln Glu Leu
 50 55 60

 Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln Ala Arg Val Thr
 65 70 75 80

 Ala Ile Glu Lys Tyr Leu Gln Asp Gln Ala Arg Leu Asn Ser Trp Gly
 85 90 95

 Cys Ala Phe Arg Gln Val Cys His Thr Thr Val Pro Trp Val Asn Asp
 100 105 110

 Ser Leu Ala Pro Asp Trp Asp Asn Met Thr Trp Gln Glu Trp Glu Lys
 115 120 125

 Gln Val Arg Tyr Leu Glu Ala Asn Ile Ser Lys Ser Leu Glu Gln Ala
 130 135 140

 Gln Ile Gln Gln Glu Lys Asn Met Tyr Glu Leu Gln Lys Leu Asn Ser
 145 150 155 160

 Trp Asp Ile Phe Gly Asn Trp Phe Asp Leu Thr Ser Trp Val Lys Asn
 165 170 175

 Tyr Ile Gln Tyr Gly Val Leu Ile Ile Val Ala Val Ile Ala Leu Arg
 180 185 190

 Ile Val Ile Tyr Val Val Gln Met Leu Ser Arg Leu Arg Lys Gly Tyr
 195 200 205

 Arg Pro Val Phe Ser Ser Pro Pro Gly Tyr Ile Gln Gln Ile His Ile
 210 215 220

 His Lys Asp Arg Gly Gln Ser Pro Ala Asn Glu Glu Thr Glu Glu Asp
 225 230 235 240

 Gly Gly Ser Asn Gly Gly Asp Arg Tyr Trp Pro Trp Pro Ile Ala Tyr
 245 250 255

 Ile His Phe Leu Ile Arg Gln Leu Ile Arg Leu Leu Thr Arg Leu Tyr
 260 265 270

 Ser Ile Cys Arg Asp Leu Leu Ser Arg Ser Phe Leu Thr Leu Gln Leu
 275 280 285

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 Gln Tyr Gly Cys Glu Trp Ile Gln Glu Ala Phe Gln Ala Ala Ala Arg
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 Ala Thr Arg Glu Thr Leu Ala Gly Ala Cys Arg Gly Leu Trp Arg Val
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Gln Gly Ala Glu Ile Ala Leu Leu
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Val Gly Ile Gly Ser Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln
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Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu
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Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu
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Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly
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Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn
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Arg Glu Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu
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Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp
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Lys Trp Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Ala
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Ala Phe Arg Gln Val Cys His Asp Arg Pro Glu Gly Ile Glu Glu Glu
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